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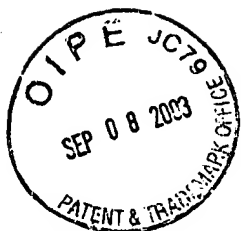
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SEQUENCE LISTING

<110> Steinaa, Lucilla
Mouritsen, Soren
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Dalum, Iben
Haaning, Jesper
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Nielsen, Klaus
Karlsson, Gunilla
Rasmussen, Peter

<120> Novel Methods for Therapeutic Vaccination

<130> 3631-0109P

<140> US 09/806,703

<141> 2001-04-04

<150> PCT/DK99/00525

<151> 1999-10-05

<150> DK 1998 01261

<151> 1998-10-05

<150> US 60/105,011

<151> 1998-10-20

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<170> PatentIn Ver. 3.0

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ctg	gcc	ctc	atc	cac	cat	aac	acc	cac	ctc	tgc	ttc	gtg	cac	acg	gtg	1440
Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	
			445					450					455			
ccc	tgg	gac	cag	ctc	ttt	cgg	aac	ccg	cac	caa	gct	ctg	ctc	cac	act	1488

Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr		
		460					465					470					
gcc	aac	cgg	cca	gag	gac	gag	tgt	gtg	ggc	gag	ggc	ctg	gcc	tgc	cac	1536	
Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His		
	475					480					485						
cag	ctg	tgc	gcc	cga	ggg	cac	tgc	tgg	ggc	cca	ggg	ccc	acc	cag	tgt	1584	
Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys		
	490					495				500					505		
gtc	aac	tgc	agc	cag	ttc	ctt	cgg	ggc	cag	gag	tgc	gtg	gag	gaa	tgc	1632	
Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys		
				510					515					520			
cga	gta	ctg	cag	ggg	ctc	ccc	agg	gag	tat	gtg	aat	gcc	agg	cac	tgt	1680	
Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys		
			525					530					535				
ttg	ccg	tgc	cac	cct	gag	tgt	cag	ccc	cag	aat	ggc	tca	gtg	acc	tgt	1728	
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys		
		540					545					550					
ttt	gga	ccg	gag	gct	gac	cag	tgt	gtg	gcc	tgt	gcc	cac	tat	aag	gac	1776	
Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp		
	555					560					565						
cct	ccc	ttc	tgc	gtg	gcc	cgc	tgc	ccc	agc	ggc	gtg	aaa	cct	gac	ctc	1824	
Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu		
	570				575					580					585		
tcc	tac	atg	ccc	atc	tgg	aag	ttt	cca	gat	gag	gag	ggc	gca	tgc	cag	1872	
Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln		
				590					595					600			
cct	tgc	ccc	atc	aac	tgc	acc	cac	tcc	tgt	gtg	gac	ctg	gat	gac	aag	1920	
Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys		
			605					610					615				
ggc	tgc	ccc	gcc	gag	cag	aga	gcc	agc	cct	ctg	acg	tcc	atc	gtc	tct	1968	
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Ile	Val	Ser		
		620					625					630					
gcg	gtg	gtt	ggc	att	ctg	ctg	gtc	gtg	gtc	ttg	ggg	gtg	gtc	ttt	ggg	2016	
Ala	Val	Val	Gly	Ile	Leu	Leu	Val	Val	Val	Leu	Gly	Val	Val	Phe	Gly		
	635					640					645						
atc	ctc	atc	aag	cga	cgg	cag	cag	aag	atc	cgg	aag	tac	acg	atg	cgg	2064	
Ile	Leu	Ile	Lys	Arg	Arg	Gln	Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met	Arg		
	650				655					660					665		
aga	ctg	ctg	cag	gaa	acg	gag	ctg	gtg	gag	ccg	ctg	aca	cct	agc	gga	2112	
Arg	Leu	Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly		
			670						675					680			
gcg	atg	ccc	aac	cag	gcg	cag	atg	cgg	atc	ctg	aaa	gag	acg	gag	ctg	2160	
Ala	Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu		
			685					690					695				
agg	aag	gtg	aag	gtg	ctt	gga	tct	ggc	gct	ttt	ggc	aca	gtc	tac	aag	2208	
Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys		
		700					705					710					
ggc	atc	tgg	atc	cct	gat	ggg	gag	aat	gtg	aaa	att	cca	gtg	gcc	atc	2256	
Gly	Ile	Trp	Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala	Ile		
	715					720					725						
aaa	gtg	ttg	agg	gaa	aac	aca	tcc	ccc	aaa	gcc	aac	aaa	gaa	atc	tta	2304	
Lys	Val	Leu	Arg	Glu	Asn	Thr	Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu		
	730				735					740					745		
gac	gaa	gca	tac	gtg	atg	gct	ggc	gtg	ggc	tcc	cca	tat	gtc	tcc	cgc	2352	
Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	Tyr	Val	Ser	Arg		
				750					755					760			
ctt	ctg	ggc	atc	tgc	ctg	aca	tcc	acg	gtg	cag	ctg	gtg	aca	cag	ctt	2400	

gac ctg gga atg ggg gca gcc aag ggg ctg caa agc ctc ccc aca cat	3312
Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His	
1070 1075 1080	
gac ccc agc cct cta cag cgg tac agt gag gac ccc aca gta ccc ctg	3360
Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu	
1085 1090 1095	
ccc tct gag act gat ggc tac gtt gcc ccc ctg acc tgc agc ccc cag	3408
Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln	
1100 1105 1110	
cct gaa tat gtg aac cag cca gat gtt cgg ccc cag ccc cct tcg ccc	3456
Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro	
1115 1120 1125	
cga gag ggc cct ctg cct gct gcc cga cct gct ggt gcc act ctg gaa	3504
Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu	
1130 1135 1140 1145	
agg gcc aag act ctc tcc cca ggg aag aat ggg gtc gtc aaa gac gtt	3552
Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val	
1150 1155 1160	
ttt gcc ttt ggg ggt gcc gtg gag aac ccc gag tac ttg aca ccc cag	3600
Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln	
1165 1170 1175	
gga gga gct gcc cct cag ccc cac cct cct cct gcc ttc agc cca gcc	3648
Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala	
1180 1185 1190	
ttc gac aac ctc tat tac tgg gac cag gac cca cca gag cgg ggg gct	3696
Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala	
1195 1200 1205	
cca ccc agc acc ttc aaa ggg aca cct acg gca gag aac cca gag tac	3744
Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr	
1210 1215 1220 1225	
ctg ggt ctg gac gtg cca gtg tga	3768
Leu Gly Leu Asp Val Pro Val	
1230	

<210> 4

<211> 1255

<212> PRT

<213> Homo sapiens

<400> 4

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu	
-20 -15 -10	
Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys	
-5 -1 1 5	
Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His	
10 15 20 25	
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr	
30 35 40	
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val	
45 50 55	
Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu	
60 65 70	
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr	
75 80 85	
Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro	
90 95 100 105	

Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	110	115	120
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	125	130	135
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	140	145	150
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	155	160	165
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	170	175	180
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	190	195	200
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	205	210	215
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	220	225	230
His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	235	240	245
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	250	255	260
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu	270	275	280
Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	285	290	295
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	300	305	310
Pro	Cys	Ala	Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	315	320	325
Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	330	335	340
Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	350	355	360
Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	365	370	375
Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	380	385	390
Asp	Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	395	400	405
Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	410	415	420
Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly	430	435	440
Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	445	450	455
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	460	465	470
Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	475	480	485
Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	490	495	500
Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys	510	515	520
Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys	525	530	535
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	540	545	550
Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp			

555	560	565
Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu		
571	575	580
Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln		585
	590	595
Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys		600
	605	610
Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Val Ser		615
	620	625
Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly		630
	635	640
Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg		645
650	655	660
Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly		665
	670	675
Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu		680
	685	690
Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys		695
	700	705
Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile		710
	715	720
Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu		725
730	735	740
Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg		745
	750	755
Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu		760
	765	770
Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg		775
	780	785
Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly		790
	795	800
Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala		805
810	815	820
Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe		825
	830	835
Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp		840
	845	850
Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg		855
	860	865
Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val		870
	875	880
Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala		885
890	895	900
Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro		905
	910	915
Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met		920
	925	930
Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe		935
	940	945
Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu		950
	955	960
Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu		965
970	975	980
Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu		985
	990	995
Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly		1000
	1005	1010
		1015

Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly
 1020 1025 1030
 Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
 1035 1040 1045
 Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
 1050 1055 1060 1065
 Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
 1070 1075 1080
 Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
 1085 1090 1095
 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
 1100 1105 1110
 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
 1115 1120 1125
 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
 1130 1135 1140 1145
 Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
 1150 1155 1160
 Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
 1165 1170 1175
 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
 1180 1185 1190
 Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
 1195 1200 1205
 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
 1210 1215 1220 1225
 Leu Gly Leu Asp Val Pro Val
 1230

<210> 5
 <211> 648
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(648)

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 Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15
 gtt ctc tgc ctc caa gcc cag gta act gtt cag tcc tca cct aat ttt 96
 Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30
 aca cag cat gtg agg gag cag agc ctg gtg acg gat cag ctc agc cgc 144
 Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
 35 40 45
 cgc ctc atc cgg acc tac cag ctc tac agc cgc acc agc ggg aag cac 192
 Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
 50 55 60
 gtg cag gtc ctg gcc aac aag cgc atc aac gcc atg gca gaa gac gga 240
 Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
 65 70 75 80
 gac ccc ttc gcg aag ctc att gtg gag acc gat act ttt gga agc aga 288
 Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg

	85	90	95	
gtc cga gtt cgc ggc gca gag aca ggt ctc tac atc tgc atg aac aag				336
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys				
	100	105	110	
aag ggg aag cta att gcc aag agc aac ggc aaa ggc aag gac tgc gta				384
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val				
	115	120	125	
ttc aca gag atc gtg ctg gag aac aac tac acg gcg ctg cag aac gcc				432
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala				
	130	135	140	
aag tac gag ggc tgg tac atg gcc ttt acc cgc aag ggc cgg ccc cgc				480
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg				
	145	150	155	160
aag ggc tcc aag acg cgc cag cat cag cgc gag gtg cac ttc atg aag				528
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys				
	165	170	175	
cgc ctg ccg cgg ggc cac cac acc acc gag cag agc ctg cgc ttc gag				576
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu				
	180	185	190	
ttc ctc aac tac ccg ccc ttc acg cgc agc ctg cgc ggc agc cag agg				624
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg				
	195	200	205	
act tgg gcc ccg gag ccc cga tag				648
Thr Trp Ala Pro Glu Pro Arg				
	210	215		

<210> 6

<211> 215

<212> PRT

<213> Homo sapiens

<400> 6

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu				
1 5 10 15				
Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe				
20 25 30				
Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg				
35 40 45				
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His				
50 55 60				
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly				
65 70 75 80				
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg				
85 90 95				
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys				
100 105 110				
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val				
115 120 125				
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala				
130 135 140				
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg				
145 150 155 160				
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys				
165 170 175				
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu				
180 185 190				

Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
 195 200 205
 Thr Trp Ala Pro Glu Pro Arg
 210 215

<210> 7
 <211> 2256
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(2256)

<400> 7
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 Met Trp Asn Ala Leu Gln Asp Arg Asp Ser Ala Glu Val Leu Gly His
 1 5 10 15
 cgc cag cgc tgg ctc cgt gtt ggg aca ctg gtg ctg gct tta acc gga 96
 Arg Gln Arg Trp Leu Arg Val Gly Thr Leu Val Leu Ala Leu Thr Gly
 20 25 30
 acc ttc ctc att ggc ttc ctc ttt ggg tgg ttt ata aaa cct tcc aat 144
 Thr Phe Leu Ile Gly Phe Leu Phe Gly Trp Phe Ile Lys Pro Ser Asn
 35 40 45
 gaa gct act ggt aat gtt tcc cat tct ggc atg aag aag gag ttt ttg 192
 Glu Ala Thr Gly Asn Val Ser His Ser Gly Met Lys Lys Glu Phe Leu
 50 55 60
 cat gaa ttg aag gct gag aac atc aaa aaa ttt tta tac aat ttc aca 240
 His Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr
 65 70 75 80
 cgg aca cca cac ttg gca gga aca caa aat aat ttt gag ctt gca aag 288
 Arg Thr Pro His Leu Ala Gly Thr Gln Asn Asn Phe Glu Leu Ala Lys
 85 90 95
 caa att cat gac cag tgg aaa gaa ttt ggc ctg gat ttg gtt gag tta 336
 Gln Ile His Asp Gln Trp Lys Glu Phe Gly Leu Asp Leu Val Glu Leu
 100 105 110
 tcc cat tac gat gtc ttg ctg tcc tat cca aat aaa act cat cct aac 384
 Ser His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn
 115 120 125
 tat atc tca ata att aat gaa gat gga aat gag att ttc aaa aca tca 432
 Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Lys Thr Ser
 130 135 140
 tta tct gaa cag cca ccc cca gga tat gag aat ata tca gat gta gtg 480
 Leu Ser Glu Gln Pro Pro Pro Gly Tyr Glu Asn Ile Ser Asp Val Val
 145 150 155 160
 cca cca tac agt gcc ttc tct cca caa ggg aca cca gag ggt gat cta 528
 Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly Thr Pro Glu Gly Asp Leu
 165 170 175
 gtg tat gtc aac tat gca cga act gaa gac ttc ttt aaa ctg gaa cgg 576
 Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg
 180 185 190
 gaa atg aag atc agt tgt tct ggg aag att gtg att gcc aga tat ggg 624
 Glu Met Lys Ile Ser Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly
 195 200 205
 aaa gtg ttc aga gga aat atg gtt aaa aat gct caa ctg gca ggg gca 672

Lys	Val	Phe	Arg	Gly	Asn	Met	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala		
210						215					220						
aaa	gga	atg	att	ctg	tac	tca	gac	cct	gct	gac	tac	ttt	gtt	cct	gcg	720	
Lys	Gly	Met	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Val	Pro	Ala		
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Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ala	Trp	Val		
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Ser	Thr	Glu	Trp	Ala	Glu	Glu	His	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly		
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Asp	Ser	Trp	Lys	Glu	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ile	Gly	Met	Pro		
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Thr	Val	Ala	Gln	Val	Arg	Gly	Ala	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser		
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Lys	Ser	Asn	Pro	Ile	Leu	Leu	Arg	Ile	Met	Asn	Asp	Gln	Leu	Met	Tyr		
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Leu	Glu	Arg	Ala	Phe	Ile	Asp	Pro	Leu	Gly	Leu	Pro	Gly	Arg	Pro	Phe		
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Tyr	Arg	His	Thr	Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly		
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gaa	tca	ttc	cct	ggg	att	tat	gat	gcc	ctt	ttt	gat	ata	agt	agc	aaa	2160	
Glu	Ser	Phe	Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Ser	Ser	Lys		
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Val	Asn	Ala	Ser	Lys	Ala	Trp	Asn	Glu	Val	Lys	Arg	Gln	Ile	Ser	Ile		
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<213> Mus musculus

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Asp	Ser	Trp	Lys	Glu	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ile	Gly	Met	Pro
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Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Lys
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Tyr	Glu	Leu	Val	Val	Lys	Phe	Tyr	Asp	Pro	Thr	Phe	Lys	Tyr	His	Leu
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Thr	Val	Ala	Gln	Val	Arg	Gly	Ala	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser
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Ile	Val	Leu	Pro	Phe	Asp	Cys	Gln	Ser	Tyr	Ala	Val	Ala	Leu	Lys	Lys
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Tyr	Ala	Asp	Thr	Ile	Tyr	Asn	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met
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Lys	Ala	Tyr	Met	Ile	Ser	Phe	Asp	Ser	Leu	Phe	Ser	Ala	Val	Asn	Asn
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Phe	Thr	Asp	Val	Ala	Ser	Lys	Phe	Asn	Gln	Arg	Leu	Gln	Glu	Leu	Asp
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Lys	Ser	Asn	Pro	Ile	Leu	Leu	Arg	Ile	Met	Asn	Asp	Gln	Leu	Met	Tyr
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Leu	Glu	Arg	Ala	Phe	Ile	Asp	Pro	Leu	Gly	Leu	Pro	Gly	Arg	Pro	Phe
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Tyr	Arg	His	Thr	Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly
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Glu	Ser	Phe	Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Ser	Ser	Lys
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Val	Asn	Ala	Ser	Lys	Ala	Trp	Asn	Glu	Val	Lys	Arg	Gln	Ile	Ser	Ile
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Phe	Leu	Tyr	Asn	Phe	Thr	Arg	Thr	Pro	His	Leu	Ala	Gly	Thr	Gln	Asn	
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aat	ttt	gag	ctt	gca	aag	caa	att	cat	gac	cag	tggt	aaa	gaa	ttt	ggc	144
Asn	Phe	Glu	Leu	Ala	Lys	Gln	Ile	His	Asp	Gln	Trp	Lys	Glu	Phe	Gly	
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ctg	gat	ttg	gtt	gag	tta	tcc	cat	tac	gat	gtc	ttg	ctg	tcc	tat	cca	192
Leu	Asp	Leu	Val	Glu	Leu	Ser	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	
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Glu	Ile	Phe	Lys	Thr	Ser	Leu	Ser	Glu	Gln	Pro	Pro	Pro	Gly	Tyr	Glu	
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aat	ata	tca	gat	gta	gtg	cca	cca	tac	agt	gcc	ttc	tct	cca	caa	ggg	336
Asn	Ile	Ser	Asp	Val	Val	Pro	Pro	Tyr	Ser	Ala	Phe	Ser	Pro	Gln	Gly	
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aca	cca	gag	ggt	gat	cta	gtg	tat	gtc	aac	tat	gca	cga	act	gaa	gac	384
Thr	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	
	115					120						125				
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Phe	Phe	Lys	Leu	Glu	Arg	Glu	Met	Lys	Ile	Ser	Cys	Ser	Gly	Lys	Ile	
130						135					140					
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Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Met	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	
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Asp	Tyr	Phe	Val	Pro	Ala	Val	Lys	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	
	180						185						190			
cct	gga	ggt	ggt	gtc	caa	cgt	gga	aat	gtc	tta	aat	ctt	aat	ggt	gca	624
Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly	Asn	Val	Leu	Asn	Leu	Asn	Gly	Ala	
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Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr	Pro	Ala	Asn	Glu	His	Ala	Tyr	Arg	
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Ile	Gly	Tyr	Asp	Asp	Ala	Gln	Lys	Leu	Leu	Glu	His	Met	Gly	Gly	Pro	
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His	Arg	Asp	Ala	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	
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Ala	Val	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Lys	
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gaa gga aat tac act cta aga gtt gat tgc aca cca ctg atg tac agc	1248
Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser	
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Leu Val Tyr Asn Leu Thr Lys Glu Leu Gln Ser Pro Asp Glu Gly Phe	
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Glu Gly Lys Ser Leu Tyr Asp Ser Trp Lys Glu Lys Ser Pro Ser Pro	
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Tyr Thr Lys Asn Trp Lys Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr	
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His Ser Val Tyr Glu Thr Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro	
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Thr Phe Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Ala Met Val	
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545 550 555 560	
aaa cat cca caa gaa atg aag gct tac atg ata tca ttt gat tca ctg	1728
Lys His Pro Gln Glu Met Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu	
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Phe Ser Ala Val Asn Asn Phe Thr Asp Val Ala Ser Lys Phe Asn Gln	
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Arg Leu Gln Glu Leu Asp Lys Ser Asn Pro Ile Leu Leu Arg Ile Met	
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Leu Pro Gly Arg Pro Phe Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser	
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Asn Phe Glu Leu Ala Lys Gln Ile His Asp Gln Trp Lys Glu Phe Gly
35 40 45
Leu Asp Leu Val Glu Leu Ser His Tyr Asp Val Leu Leu Ser Tyr Pro
50 55 60
Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn
65 70 75 80
Glu Ile Phe Lys Thr Ser Leu Ser Glu Gln Pro Pro Gly Tyr Glu
85 90 95
Asn Ile Ser Asp Val Val Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly
100 105 110
Thr Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp
115 120 125
Phe Phe Lys Leu Glu Arg Glu Met Lys Ile Ser Cys Ser Gly Lys Ile
130 135 140
Val Ile Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Met Val Lys Asn
145 150 155 160
Ala Gln Leu Ala Gly Ala Lys Gly Met Ile Leu Tyr Ser Asp Pro Ala
165 170 175
Asp Tyr Phe Val Pro Ala Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu
180 185 190
Pro Gly Gly Gly Val Gln Arg Gly Asn Val Leu Asn Leu Asn Gly Ala
195 200 205
Gly Asp Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu His Ala Tyr Arg
210 215 220
His Glu Leu Thr Asn Ala Val Gly Leu Pro Ser Ile Pro Val His Pro
225 230 235 240
Ile Gly Tyr Asp Asp Ala Gln Lys Leu Leu Glu His Met Gly Gly Pro
245 250 255
Ala Pro Pro Asp Ser Ser Trp Lys Gly Gly Leu Lys Val Pro Tyr Asn
260 265 270
Val Gly Pro Gly Phe Ala Gly Asn Phe Ser Thr Gln Lys Val Lys Met
275 280 285
His Ile His Ser Tyr Thr Lys Val Thr Arg Ile Tyr Asn Val Ile Gly
290 295 300
Thr Leu Lys Gly Ala Leu Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly
305 310 315 320
His Arg Asp Ala Trp Val Phe Gly Gly Ile Asp Pro Gln Ser Gly Ala
325 330 335
Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu Lys Lys Lys

<400> 11
 cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc gag ctg 45
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
 1 5 10 15

<210> 12
 <211> 15
 <212> PRT
 <213> Clostridium tetani

<400> 12
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
 1 5 10 15

<210> 13
 <211> 63
 <212> DNA
 <213> Clostridium tetani

<220>
 <221> CDS
 <222> (1)..(63)

<400> 13
 ttc aac aac ttc acc gta agc ttc tgg ctg cgt gtt ccg aaa gtt agc 48
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 1 5 10 15
 gct agc cac ctg gaa 63
 Ala Ser His Leu Glu
 20

<210> 14
 <211> 21
 <212> PRT
 <213> Clostridium tetani

<400> 14
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 1 5 10 15
 Ala Ser His Leu Glu
 20

<210> 15
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 tetanus toxoid epitope and PSM

<400> 15

Gln Glu Arg Gly Val Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu Arg Val Asp Cys Thr
20 25

<210> 16

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 16

Ala Val Val Leu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu Glu Met Lys Thr Tyr
20 25

<210> 17

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 17

Met Phe Leu Glu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu His Val Ile Tyr Ala
20 25

<210> 18

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 18

Asn Ser Arg Leu Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
1 5 10 15
Val Pro Lys Val Ser Ala Ser His Leu Glu Val Asp Cys Thr Pro
20 25 30

<210> 19
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 tetanus toxoid epitope and PSM

<400> 19
 Val Val Leu Arg Lys Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
 1 5 10 15
 Val Pro Lys Val Ser Ala Ser His Leu Glu Ser Phe Asp Ser Leu
 20 25 30

<210> 20
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 tetanus toxoid epitope and PSM

<400> 20
 Leu Met Phe Leu Glu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
 1 5 10 15
 Val Pro Lys Val Ser Ala Ser His Leu Glu Pro Ser Ser His Asn
 20 25 30

<210> 21
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial His
 tag

<220>
 <221> CDS
 <222> (1)..(18)

<400> 21
 cat cat cat cat cat cat
 His His His His His His
 1 5

18

<210> 22
 <211> 6

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial His
tag

<400> 22

His His His His His His
1 5

<210> 23

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial His
tag

<220>

<221> CDS

<222> (1)..(42)

<400> 23

atg aaa cac caa cac caa cat caa cat caa cat caa cat caa
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln
1 5 10

42

<210> 24

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial His
tag

<400> 24

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln
1 5 10

<210> 25

<211> 69

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(69)

<400> 25

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga 48
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15

gca gtc ttc gtt tgg ccc agc 69
 Ala Val Phe Val Ser Pro Ser
 20

<210> 26
 <211> 23
 <212> PRT
 <213> Mus musculus

<400> 26
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser
 20

<210> 27
 <211> 33
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(33)

<400> 27 33
 gaa caa aaa ctc atc tca gaa gag gat ctg aat
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 1 5 10

<210> 28
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 28
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 1 5 10

<210> 29
 <211> 75
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(75)

<400> 29 48
 atg aag gat tcc tgc atc act gtg atg gcc atg gcg ctg ctg tct ggg

Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly
 1 5 10 15
 ttc ttt ttc ttc gcg ccg gcc tcg agc 75
 Phe Phe Phe Phe Ala Pro Ala Ser Ser
 20 25

<210> 30
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly
 1 5 10 15
 Phe Phe Phe Phe Ala Pro Ala Ser Ser
 20 25

<210> 31
 <211> 60
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(60)

<400> 31
 atg aga agg atg ctt ctg cac ttg agt gtt ctg act ctc agc tgt gtc 48
 Met Arg Arg Met Leu Leu His Leu Ser Val Leu Thr Leu Ser Cys Val
 1 5 10 15
 tgg gcc act gcc 60
 Trp Ala Thr Ala
 20

<210> 32
 <211> 20
 <212> PRT
 <213> Mus musculus

<400> 32
 Met Arg Arg Met Leu Leu His Leu Ser Val Leu Thr Leu Ser Cys Val
 1 5 10 15
 Trp Ala Thr Ala
 20

<210> 33
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 33
 Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala

<400> 35

```
Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
1      5      10      15
Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
20      25      30
Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
35      40      45
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
50      55      60
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
65      70      75      80
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
85      90      95
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
100     105     110
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
115     120     125
Phe Thr Glu Ile Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
130     135     140
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
145     150     155     160
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
165     170     175
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
180     185     190
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
195     200     205
Thr Trp Ala Pro Glu Pro Arg
210     215
```

<210> 36

<211> 195

<212> PRT

<213> Artificial Sequence

<220>

<223> Fig. 6 - F30N: Variant of FGF8b with P30 epitope in the N-terminal

<400> 36

```
Met Ala Gln Val Thr Val Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
1      5      10      15
Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Arg Arg Leu Ile Arg
20      25      30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
35      40      45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
50      55      60
Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65      70      75      80
Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
85      90      95
Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu Ile
100     105     110
Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu Gly
115     120     125
Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys
```


130		135		140
Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro Arg				
145		150		155
Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn Tyr				
	165		170	175
Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp Ala Pro				
	180		185	190
Glu Pro Arg				
195				

<210> 37
 <211> 208
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Fig. 6 - F2I: Internal variant of FGF8b constructed by replacing external loops in the FGF2 structure with P2 epitope

<400> 37	
Met Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val	
1	5 10 15
Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg	
	20 25 30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu	
	35 40 45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala	
	50 55 60
Lys Leu Ile Val Glu Thr Asp Gln Tyr Ile Lys Ala Asn Ser Lys Phe	
65	70 75 80
Ile Gly Ile Thr Glu Leu Gly Ser Arg Val Arg Val Arg Gly Ala Glu	
	85 90 95
Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu Ile Ala Lys	
	100 105 110
Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu Ile Gly Leu Glu	
	115 120 125
Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu Gly Trp Tyr Met	
	130 135 140
Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys Thr Arg Gln	
145	150 155 160
His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro Arg Gly His His	
	165 170 175
Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn Tyr Pro Pro Phe	
	180 185 190
Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp Ala Pro Glu Pro Arg	
	195 200 205

<210> 38
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Fig. 6 - F30I: Internal variant of FGF8b constructed by replacing

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external loops in the EGF2 structure with P30 epitope

<400> 38

```

Met Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val
1      5      10      15
Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg
      20      25      30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
      35      40      45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
      50      55      60
Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65      70      75      80
Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
      85      90      95
Ile Ala Lys Ser Asn Gly Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
      100     105     110
Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Asp Cys Val Phe Thr
      115     120     125
Glu Ile Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr
      130     135     140
Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly
145     150     155     160
Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu
      165     170     175
Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu
      180     185     190
Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp
      195     200     205
Ala Pro Glu Pro Arg
      210

```

<210> 39

<211> 199

<212> PRT

<213> Artificial Sequence

<220>

<223> Fig. 6 -F2C: Variant of FGF8b with P2 epitope in the C-terminal

<400> 39

```

Met Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val
1      5      10      15
Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg
      20      25      30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
      35      40      45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
      50      55      60
Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65      70      75      80
Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
      85      90      95
Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu Ile
      100     105     110

```

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Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu Gly
 115 120 125
 Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys
 130 135 140
 Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro Arg
 145 150 155 160
 Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn Tyr
 165 170 175
 Pro Pro Phe Thr Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
 180 185 190
 Thr Glu Leu Pro Glu Pro Arg
 195

<210> 40
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A preferred pan DR epitope (PADRE) peptide has this sequence
 <400> 40

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
 1 5 10

<210> 41
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FGF8b specific peptide
 <400> 41

Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr
 1 5 10